

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 16:29:19 ; Search time 6370.22 Seconds
(without alignments)
10058.575 Million cell updates/sec

Title: US-10-814-760A-2
Perfect score: 1002
Sequence: 1 gcggagggagtggaaggctc.....cagtacatattggaggggcg 1002

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

POMC

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1002	100.0	1002	14	BOVPOMC7 J00021 Bovine proo
2	840.8	83.9	1083	14	BTBLPH V00107 Bovine mRNA
3	838.6	83.7	1084	14	BOVACTH M25587 Bovine cort
4	763.2	76.2	793	14	BOVBPH M23814 Bos taurus
5	722.4	72.1	732	14	BOVPOMCFR M38606 Bovine proo
6	629.8	62.9	792	14	OAR507201 AJ507201 Ovis arie
7	570.6	56.9	1097	14	SSPOM1 X00135 Porcine pro
8	570	56.9	1042	14	SSPOMCR X03561 Pig mRNA fo
9	537.4	53.6	995	14	S73519 S73519 pro-opiomel
10	463.4	46.2	8658	5	HSACTH V01510 H.sapiens g

	11	462.4	46.1	1230	5	HUMPOMC9	J00292 Human proop
c	12	462.4	46.1	95214	5	AC012457	AC012457 Homo sapi
	13	457.8	45.7	1115	5	MACPOMCA	M19658 Macaca neme
	14	457	45.6	1078	5	BC065832	BC065832 Homo sapi
	15	456	45.5	1050	2	CQ720465	CQ720465 Sequence
	16	438.2	43.7	908	5	HUMPOMCZ	M38297 Human proop
	17	432.8	43.2	663	14	AY024339	AY024339 Canis fam
	18	413.4	41.3	804	5	BT019918	BT019918 Homo sapi
	19	413.4	41.3	804	8	AY888671	AY888671 Synthetic
	20	413.2	41.2	936	2	AX534756	AX534756 Sequence
	21	412.4	41.2	804	8	AY893864	AY893864 Synthetic
	22	410.8	41.0	801	5	CR541826	CR541826 Homo sapi
	23	410.8	41.0	804	8	AY893863	AY893863 Synthetic
	24	409	40.8	899	6	S78260	S78260 pro-opiomel
	25	372.6	37.2	1315	2	AX463491	AX463491 Sequence
	26	360.8	36.0	585	14	MVIPOMCA	J03039 M.vison (mi
	27	325	32.4	562	5	AY091991	AY091991 Pan trogl
	28	310.6	31.0	559	5	AY091992	AY091992 Gorilla g
	29	309.8	30.9	237327	12	AC103454	AC103454 Rattus no
c	30	309.8	30.9	250999	12	AC119009	AC119009 Rattus no
	31	309.4	30.9	845	2	AR373945	AR373945 Sequence
	32	309.4	30.9	845	2	AR474303	AR474303 Sequence
	33	309.4	30.9	845	6	MUSPOMC03	J00612 Mouse proop
	34	309.4	30.9	211926	6	AC111092	AC111092 Mus muscu
	35	309	30.8	759	6	MMOPI2	V01529 Mouse gene
	36	308.2	30.8	781	6	RATPOMC3	J00759 Rat proopio
	37	307.2	30.7	1070	6	BC061215	BC061215 Mus muscu
	38	306.8	30.6	967	6	BC058443	BC058443 Rattus no
	39	303	30.2	714	6	AF510391	AF510391 Rattus no
	40	299.4	29.9	301	7	BV104815	BV104815 MARC 6319
	41	297	29.6	708	2	AX534751	AX534751 Sequence
	42	271.6	27.1	496	5	AY091993	AY091993 Pongo pyg
	43	271	27.0	490	5	AY091994	AY091994 Macaca sp
	44	267.8	26.7	490	5	AY091995	AY091995 Saguinus
	45	244.8	24.4	256	14	S57982	S57982 proopiomela

ALIGNMENTS

RESULT 1

BOVPOMC7

LOCUS BOVPOMC7 1002 bp DNA linear MAM 30-OCT-1994

DEFINITION Bovine proopiomelanocortin (POMC) gene, exon 3.

ACCESSION J00021

VERSION J00021.1 GI:163568

KEYWORDS adrenocorticotropin; alpha-melanotropin; beta-lipotropin; beta-melanotropin; corticotropin; enkephalin; gamma-lipotropin; lipotropin; melanotropin; met-enkephalin; neuropeptide Y; proopiomelanocortin.

SEGMENT 7 of 7

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 100 to 936)

AUTHORS Nakanishi,S., Inoue,A., Kita,T., Nakamura,M., Chang,A.C., Cohen,S.N. and Numa,S.

TITLE Nucleotide sequence of cloned cDNA for bovine corticotropin-beta-lipotropin precursor

JOURNAL Nature 278 (5703), 423-427 (1979)

PUBMED 221818

REFERENCE 2 (bases 82 to 140; 889 to 962)

AUTHORS Nakanishi,S., Teranishi,Y., Noda,M., Notake,M., Watanabe,Y.,

Kakidani,H., Jingami,H. and Numa,S.
 TITLE The protein-coding sequence of the bovine ACTH-beta-LPH precursor
 gene is split near the signal peptide region
 JOURNAL Nature 287 (5784), 752-755 (1980)
 PUBMED 6253815
 REFERENCE 3 (bases 1 to 1002)
 AUTHORS Nakanishi,S., Teranishi,Y., Watanabe,Y., Notake,M., Noda,M.,
 Kakidani,H., Jingami,H. and Numa,S.
 TITLE Isolation and characterization of the bovine
 corticotropin/beta-lipotropin precursor gene
 JOURNAL Eur. J. Biochem. 115 (3), 429-438 (1981)
 PUBMED 6263630
 COMMENT Original source text: Bovine calf thymus DNA [2],[3] and cDNA to
 mRNA [1].
 The POMC gene region is approximately 7.3 kb in length, coding for
 corticotropin (ACTH), beta-lipotropin (beta-LPH) and their
 component peptides which independently possess biological activity.
 The region consists of three exons divided by two large introns.
 Repetitive sequences are found in the 5' flanking segment and in
 each of the introns. Exon 3, according to [2], contains the gene
 sequence for most of the protein structure, including the known
 biologically active component peptides. [1] reports the boundaries
 of the mature peptides.
 FEATURES Location/Qualifiers
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ORIGIN about 420 bp after <bovpomc6>; 57 bp upstream of BstNI site.

Query Match 100.0%; Score 1002; DB 14; Length 1002;
 Best Local Similarity 100.0%; Pred. No. 2.4e-249;
 Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCGGAGGGAGTGGAAGGCTCAGGCGGCGCGCTTGAGGGGCGGGTGAACGCCCGGCCTGG 60
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Db      1 GCGGAGGGAGTGGAAGGCTCAGGCGGCGCGCTTGAGGGGCGGGTGAACGCCCGGCCTGG 60

Qy     61 AGTGGGCGGGGCTGACGCGCTCTGCCGCTCTCCGCAGGCGTGCATCCGGGCTGCAAGC 120
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Qy    121 CCGACCTCTCCGCCGAGACGCCGGTGTTCGCCGCAACGGCGATGAGCAGCCGCTGACTG 180
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Qy    181 AGAACCCCGGAAGTACGTACATGGGCCATTTCCGCTGGGACCGCTTCGGCCGTCGGAATG 240
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Qy    241 GTAGCAGCAGCAGCGGAGTTGGGGGCGCGGCCAGAAAGCGCAGGAGGAAGTGGCGGTGG 300
         |||
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Qy    301 GCGAAGGCCCGGGCCCCGCGGCGATGACGCCGAGACGGGTCCGCGCGAGGACAAGCGTT 360
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Qy    361 CTTACTCCATGGAACACTTCCGCTGGGGCAAGCCGGTGGGCAAGAAGCGGCGCCCGGTGA 420
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Qy	421	AGGTGTACCCCAACGGCGCCGAGGACGAGTCGGGCCAGGCCTTTCCCTCGAATTCAAGA	480
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Qy	481	GGGAGCTGACCGGGGAGAGGCTCGAGCAGGCGCGCGGCCCGAGGCCAGGCTGAGAGTG	540
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Qy	601	AGAAGAAGGACTCGGGGCCCTATAAGATGGAACACTTCCGCTGGGGCAGCCCCGCCAAGG	660
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Qy	661	ACAAGCGCTACGGCGGGTTCATGACCTCCGAGAAGAGCCAAACGCCCTTGTACGCTGT	720
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Qy	721	TCAAAAACGCCATCATCAAGAACGCCCAAGAAGGGCCAGTGAGGGCGCAGCGGGCAGG	780
Db	721	TCAAAAACGCCATCATCAAGAACGCCCAAGAAGGGCCAGTGAGGGCGCAGCGGGCAGG	780
Qy	781	GGCCTCTCTCCGCGGAAAGTTGACCCTGAAGGCCTCTCTTCTGCCCTCCTACCGCCTCGC	840
Db	781	GGCCTCTCTCCGCGGAAAGTTGACCCTGAAGGCCTCTCTTCTGCCCTCCTACCGCCTCGC	840
Qy	841	AGCCTGGGTGAGGATTGCGCCAGGCAGTGATGGCGCCAGGTATCCCGACTCTTAAAGCTG	900
Db	841	AGCCTGGGTGAGGATTGCGCCAGGCAGTGATGGCGCCAGGTATCCCGACTCTTAAAGCTG	900
Qy	901	TCTGTAGTTAAGAAATAAAACCTTTCAAGTTTCACGAATATTGACTGGGTGAATTAAAAA	960
Db	901	TCTGTAGTTAAGAAATAAAACCTTTCAAGTTTCACGAATATTGACTGGGTGAATTAAAAA	960
Qy	961	CGCATTTCCATCAAGTAAAGGGCAGTACATATTGGAGGGGCG	1002
Db	961	CGCATTTCCATCAAGTAAAGGGCAGTACATATTGGAGGGGCG	1002